

This listing of claims will replace all prior versions and listings of claims in the application.

Listing of Claims

1. (Currently amended) A method of identifying a base at a target position in a sample nucleic acid sequence wherein a primer, which hybridizes to the sample nucleic acid immediately adjacent to the target position, is provided and the sample nucleic acid and primer are subjected to a polymerase reaction in the presence of a nucleotide whereby the nucleotide will only become incorporated if it is complementary to the base in the target position, and said incorporation is detected, whereby detection of incorporation of said nucleotide is indicative of identification of a base at a target position that is complementary to said nucleotide, characterized in that, a single-stranded nucleic acid binding protein is included in the polymerase reaction step, and is added after hybridization of the primer to the sample nucleic acid.
2. (Original) A method as claimed in claim 1 wherein the single-stranded nucleic acid binding protein is selected from the group comprising *E. coli* single-stranded binding protein (Eco SSB), T4 gene 32 protein (T4 gp32), T7 SSB, coliphage N4 SSB, T4 gene 44/62 protein, adenovirus DNA binding protein (AdDBP or AdSSB) and calf thymus unwinding protein (UP1).
3. (Original) A method as claimed in claim 2 wherein the single-stranded nucleic acid binding protein is Eco SSB.
4. (Previously amended) A method as claimed in claim 1 wherein the sample nucleic acid is DNA.
5. (Previously amended) A method as claimed in claim 1 wherein the single-stranded nucleic acid binding protein binds to the sample nucleic acid.
6. (Previously amended) A method as claimed in claim 1 wherein the incorporation of the nucleotide is detected by monitoring the release of inorganic pyrophosphate.

7. (Original) A method as claimed in claim 6 wherein the release of inorganic pyrophosphate is detected using ATP sulphurylase and luciferase.

8. (Previously amended) A method as claimed in claim 1 wherein apyrase is present during the polymerase reaction.

9. (Cancelled).

10. (Previously amended) A method as claimed in claim 1 wherein at least 25 bases in the nucleic acid sample are identified.

11-14. (Cancelled).

15. (Original) A kit for use in a method of sequencing-by-synthesis which comprises nucleotides for incorporation, a polymerase, means for detection of incorporation and a single-stranded nucleic acid binding protein.